

FIG. 1A

006T50" sh6h2560

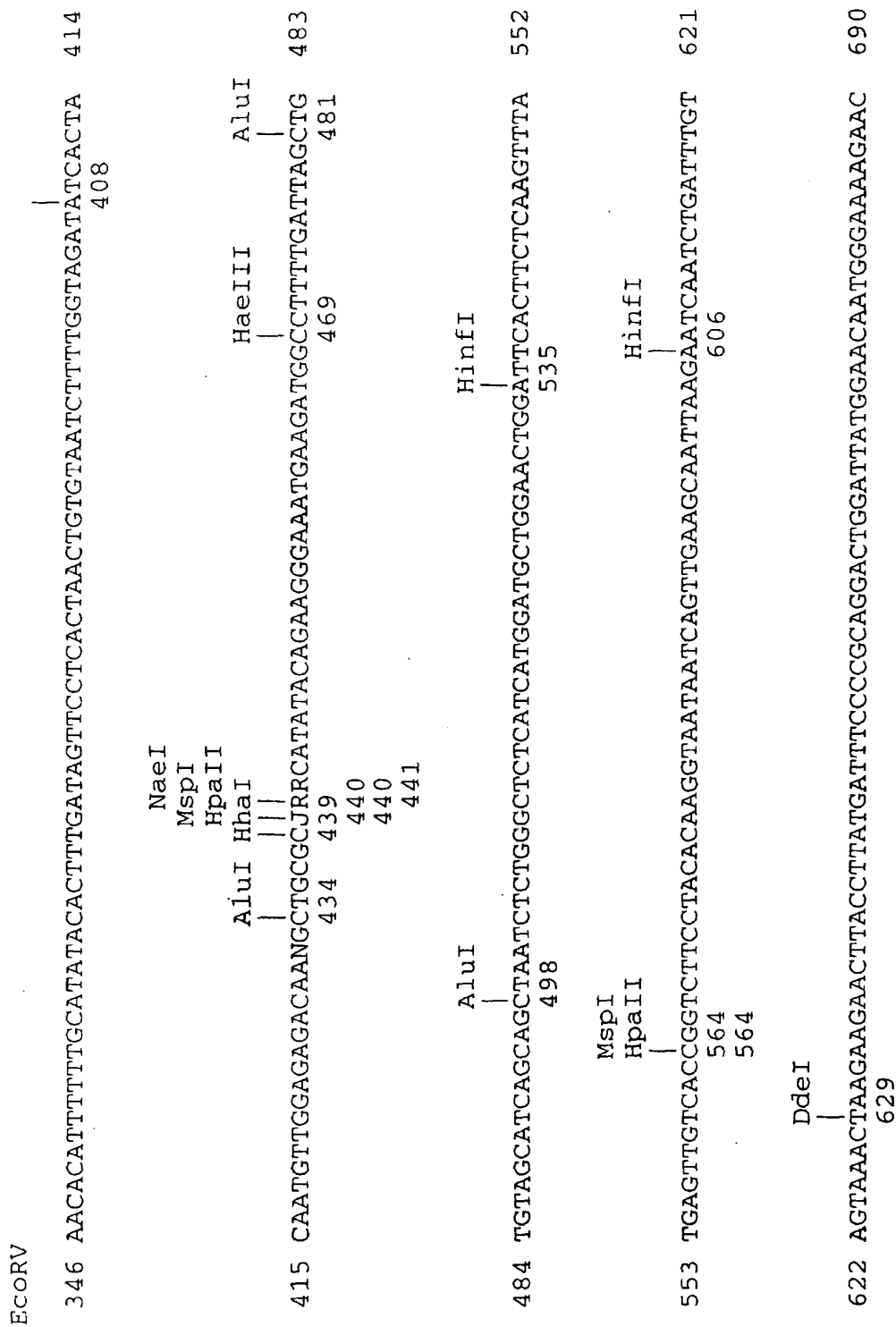


FIG. 1B

DDTSD" 5764560

SacI
AluI
702
691 TACTATATAAGCTCCATAGCGGGTTCAGATAAACGGGAGCTCTTTTAGTTGTATGTCAAAAAGGTTAGTGT 759
729
731
AluI
760 TTAGTGAATAAATAAACTTATTATCAAAAAGTCTTCATTGACTTATTTATATACTTGTGTGAATTGGTA 828
DdeI
843
829 GGAAC TACTTATTTCTCAGCAGTCATACAAAAGTGAGTGAGTCACTCATTTCCATTCAAGTGGATAAATAAGAAA 897
866
HinfI
XmnI
909
898 TGGAAAAGAAGATTTTTCATGTAAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGG 966
962
TaqI
967 AACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTATTTTATTTCCCTGATAG 1035
982
982
Sau3AI
BclI
1036 TCTAATAATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTGTACCCCAAGCGATGGGATA 1104
1075
1088
AluI
RsaI

FIG. 1C

CCGAGCAATTGGAGCGGAGCCTCAGGGTCGTCATAATACCAATCAAGACGTAACCAAGCAGT

1105 CATAGGAGGTGGAGAAATGGGTATAGATAAATCAATGGCAGCAACTCCGGATCAAGCAGCTTTCATA 1173
Sau3AI AluI
1156 1166

1174 TTAAGCATACCAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCCACCACCGCCTTCCAAAGT 1242
HinfI
1216

1243 ACTCATGTCAAGGTGGTTTCTTTAGCTTTTGAACACAGATTGGGATCTTTTGTGTTTGTTCATATAC 1311
ScaI RsaI AluI Sau3AI
1243 1269 1286

1312 ATAGGACCTGAGAGCTTTTGGTTGAATTTTTTTTTTCAGGACAAATGGGCCGAAGAAATCTGTACATTG 1380
DdeI DdeI AluI HinfI RsaI
1316 1326 1368 1375

1381 CATCAATATGCTATGGCAGGACAGTGTGCTGATGATACACACTTAAGCATCATGTGTGTAGAAAG 1449
MstII DdeI
1472 1472

1450 CCGAAGACAATTGGAGCGGAGCCTCAGGGTCGTCATAATACCAATCAAGACGTAACCAAGCAGCAGTC 1518
Tth111I
1514

FIG. 1D

006750-04042500

1519 TCTTTGGTTGAATGTGATGAAAGGGATGTGTCTTGGTATGTATGTACGAGTAACAAAGAGAAGATGCA 1587
1564
RsaI |

1588 ATTGAGTAGTAGAAAGATTGTGAGAGCTTTTAAAGCCCTTCAAGTGTGTGCTTTTATCTTATCGATATC 1656
1613 1619
AluI | DraI | EcoRV |

1657 ATCCATTGCGTGTGTTAATGCGTCTTTAGATATGTTTCTGTGTTTCTTCTCAGTGTCTGAATATCTGAT 1725
1706
DdeI |

1726 AAGTGCAATGTGAGAAAGCCACACCAAAATATTCAAATCTTATATTTTTTAATAATGTCGAATCA 1794
1790
1788
TagI | HinfI |

1795 CTCGGAGTTGCCACCTTCTGTGCCAATTGTGCTGAATCTATCACACTAAAAAACAATTTCTTCAAGGT 1863
1829
HinfI |

1864 AATGACTTGTGGACTATGTTCTGGAATTCATTAAGTTTTTATTTTTTGAAGTTTAAGTTTTTACCTTC 1932
1887
EcoRI |

FIG. 1E

006750-94642560

1933 TTTTTTGA AAAAATATCGTTTCATAAGATGTCACGCCAGGACATGAGCTACACATCACATATTAGCATGCA 2001
1968 1978 SphI

2002 GATGCGGACGATTTGTCACTCACTTCAAACACCTAAAGAGCTTCTCTCTCACAGCACACACATATG 2070
2043 2067 NdeI

2071 CATGCAATATTTACACGTTGATCGCCATGCAAAATCTCCATTCTCACCTATAAATTAGAGGCTCGGCTTCA 2139
2073 2075

2140 CTTTTTACTCAAAACCAAACTCATCACTACAAAACATACACAAATGGCGAACAAGCTCTTC 2200
Met 2195 AluI

FIG. 1F

[illegible]

FIGURE 2A

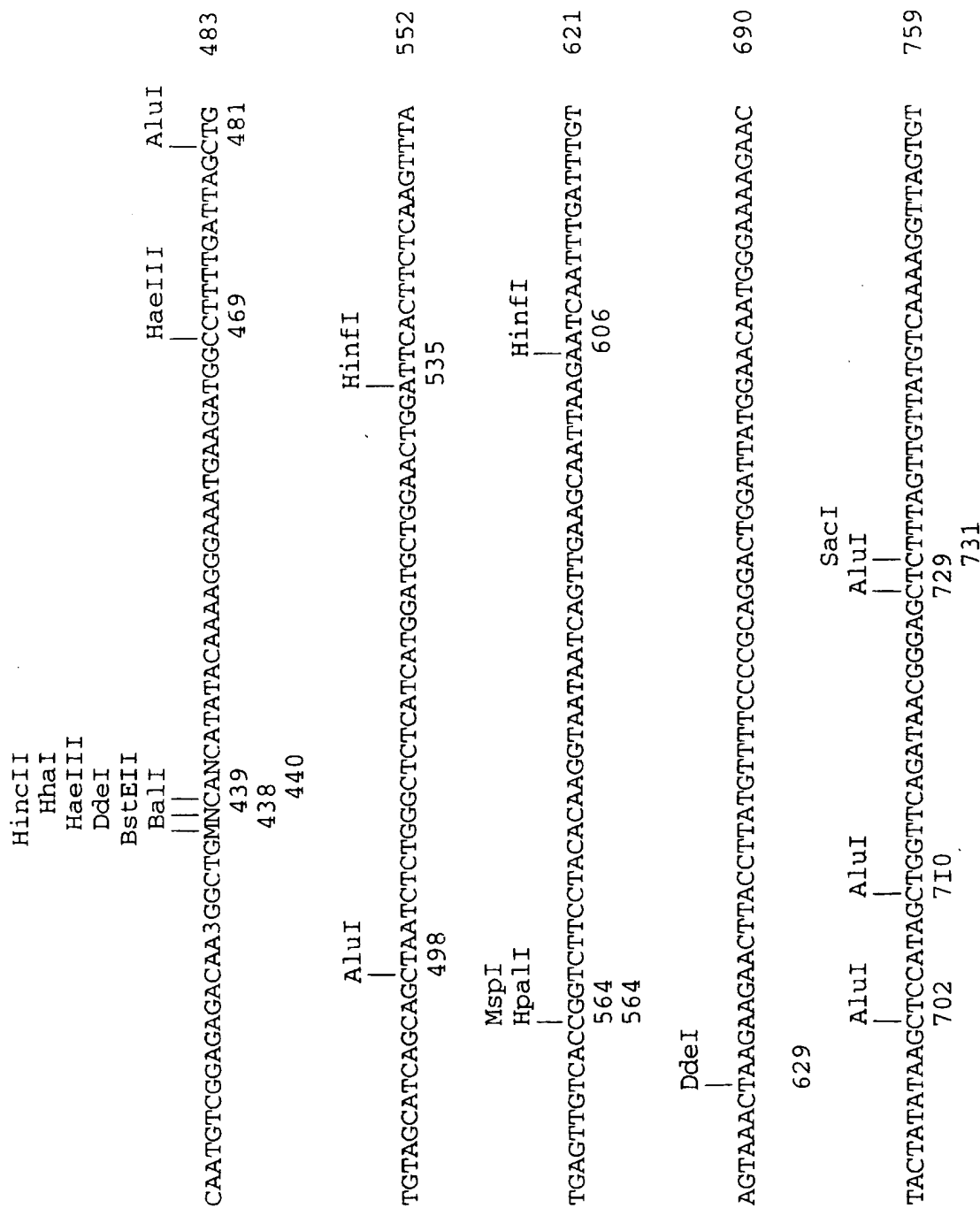


FIGURE 2B

006F50" 94642360

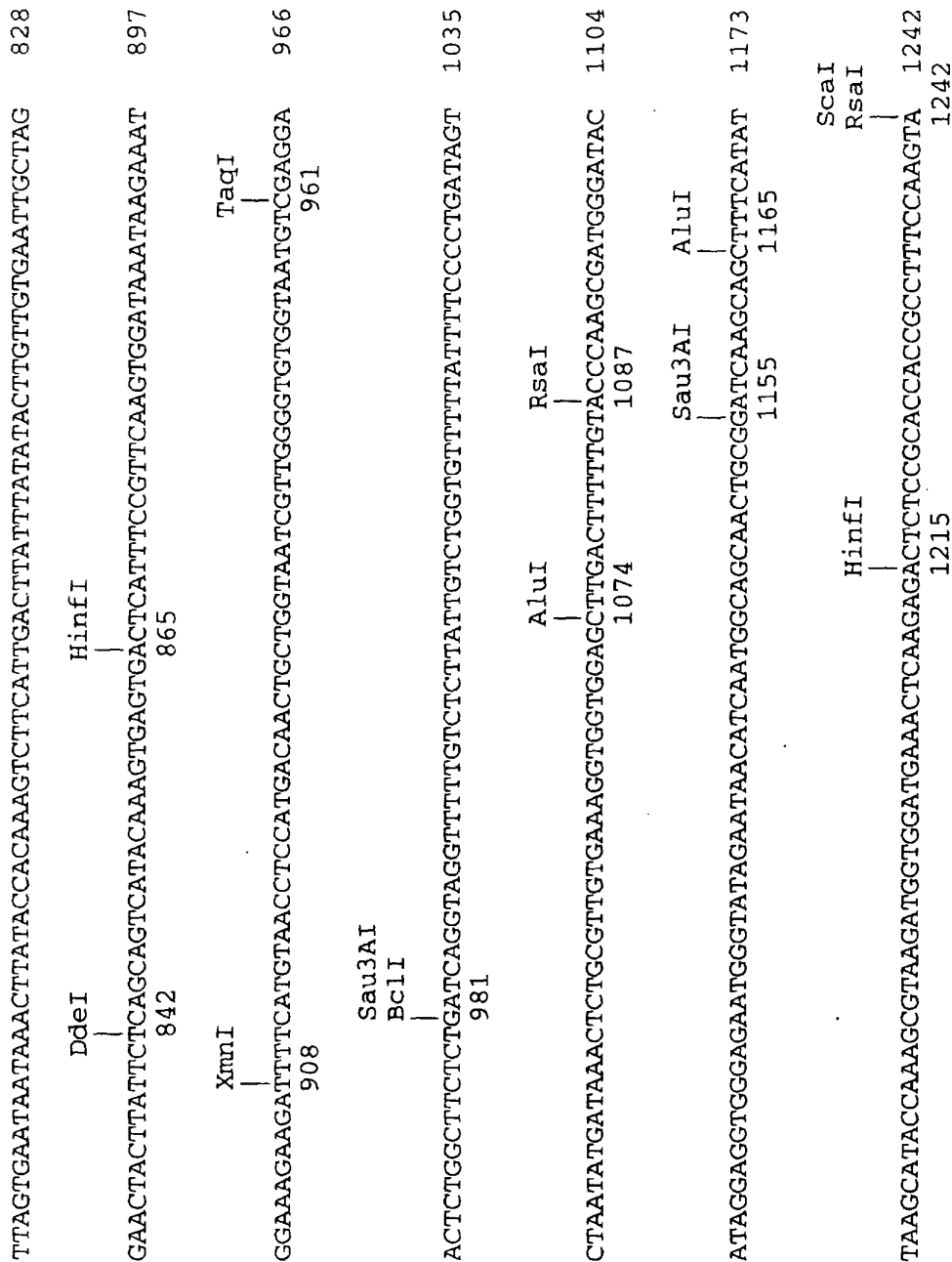


FIGURE 2C

[illegible]

FIGURE 2D

FIGURE 2E

FIGURE 2E

006T50" 9thh2560

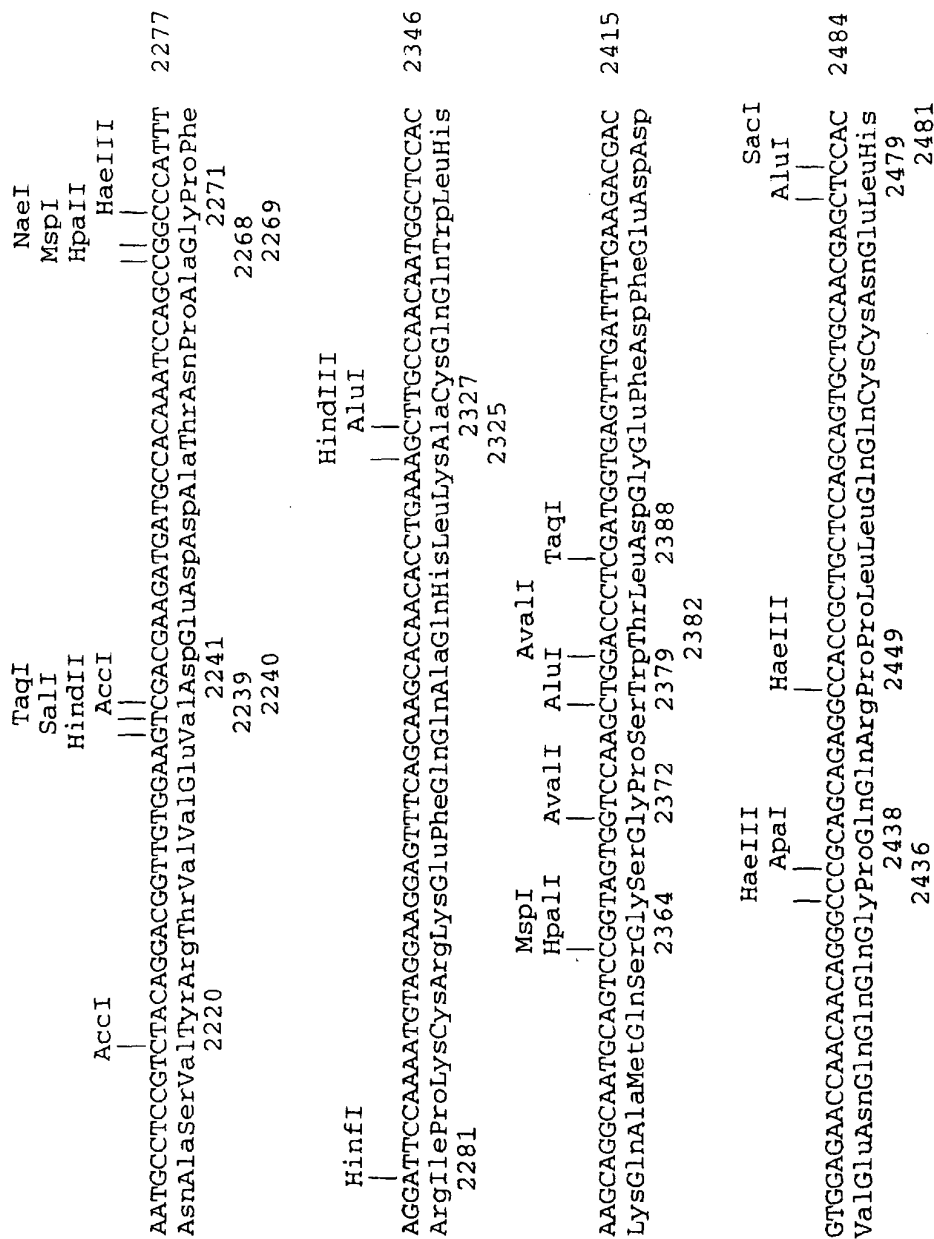


FIGURE 2F

006F50" 91644560

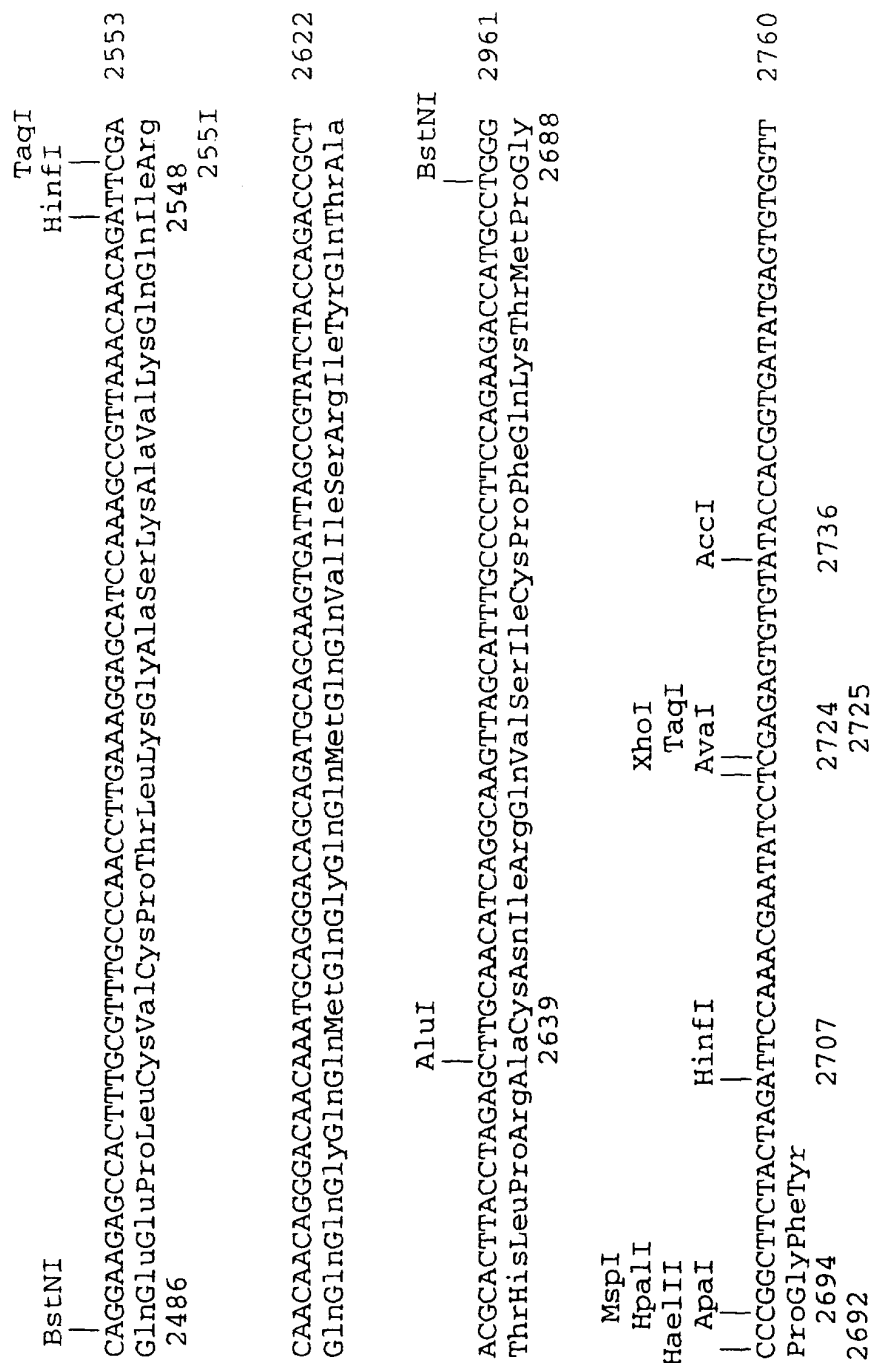


FIGURE 2G

G06F 50/00 (20060101)

HindII
|
GTTGATGTATGTTAAACACTACATAGTCATGGTGTGTTCCATAAATAATGTACTAATGTAATAAGAAC 2829
2771 RsaI
|
2813

AccI
|
TACTCCGTAGACGGTAATAAAAGAGAGAGTTTTTTTTTACTCTTGCTACTTTCCTATATAAGTGATGAT 2898
2838

ScaI
RsaI
|
TAACAACAGATACACCAAAAGAAAAACAATTAATCTATATTCACAATGAAGCAGTACTAGTCTATTGAA 2967
2954

Sau3AI
|
CATGTCAGATTTTCTTTTCTAAATGTCTAATTAAGCCTTCAAGGCTAGTGTATGATAAAAGATCATCCA 3036
3028

Sau3AI
BamHI
|
ATGGGATCCAACAAGACTCCTCAAAATCTGGTTTTTGATCAGATACTTCAAAACTATTTTTTGTATTCAATTAAA 3105
3041 3053 3069

Sau3AI
BclI
|

FIGURE 2H

G06F50-00:3642360

HinfI
|
TTATGCAAGTGTTCTTTTATTATTGGTGAAGACTCTTTAGAAAGCAAAGAACGACAGCAGTAATAAAAAA 3174
3135
ACAAAGTTCAGTTTTAAGATTGTTATTGACTTATTGTCACTTTTGAAAAATATAGTATGATATTAATATA 3243
GTTTTATTATATAATGCTTGTCTATTCAAGATTTGAGAACATTAAATATGATACTGTCCACATATCCAA 3312
NdeI
|
TATATTAAGTTTCATTCTGTTCAAACATATGATAAGATGGTCAAATGATTATGAGTTTGTATTAC 3381
3341
TaqI Sau3AI
AluI RsaI
| |
CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTATCTTCATTTCTTGGCTAAAAGCGA 3450
3402 3421
3405 3425
ATATGACATCACCTAGAGAAAGCCGATAATAGTAAACTCTGTCTCTGGTTTTTGGTTTAAATCAAACCGA 3519
MspI DdeI
HpaI AluI
| |
ACCGGTAGCTGAGTGTCAAGTCAGCAAAACATCGCAACCATATGTCAATTCTGTTAGATTCCCGGTTTAA 3588
3522 3528
3529 3576
3581

FIGURE 21

006450 34642560

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TaqI      HindIII      DdeI
|      |      |
HinfI      AluI
|      |
TCGAATCTTATTCCTGCTGCTGTTTACCGATAAAGCTTAAGACTTTATTGATAAAAGTCTCA 4002
3937      3976      4000
3935      3974

AluI      XmnI      HinfI      DdeI
|      |      |      |
GCTTTGAATGTGAATGAACCTGTTTCCTGCTTATTAGTGTTCCTTTGTTTGAGTTGAATCACTGCTCTTA 4071
4004      4023      4059      4069

HinfI
|
GCACTTTTGTTAGATTTCATCTTTGTGTTTAAAGTTAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140
4085

HincII
|
ACAAGGTTAACTTTGTGTTTATAACAGAAGTTGCCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG 4209
4146

AvalI      AluI      DdeI      Sau3AI
|      |      |      |
GACCAAGCTCTCTCAGCGGAAGATCCCTTACTTCAATGCCCCCAATCTACTTGGAACAAAGACACAGAT 4278
4210      4217      4222      4231

```

FIGURE 2K

[illegible]

FIGURE 2L

GenBank® Submission

Brassica campestris ACP Genomic Sequence

1 AAGAGTATGTTCTACTACTACTCTATAATCAAGTTTCAAGAAGCTTGAGCTTGGCTCTCAGCTTTATAT 69
11 46 51
47

70 GTTTGATGTTGTCAGGTATGGTAAATCATGGAAGAGATAAAGAATGCAACCCTGAAGTATTGG 138

139 CAGAGAGGACTGAGGTGAGAGAGCATGTCACCTTTGTGTACTCATCTGAATTATCTTATATGCGAAT 207
149

208 GTAAGTGGTACTAAAAGGTTTGTAACTTTTGGTAGGTGGATTGGAAGGATAAAATGGAGGAACCTTGCTTC 276
217

277 GGTAGCGGTAACAAGTTTATATATTGCTATGAAGCTTTTTCCTGCGTGACGTATCAGCAGCTGTGGAG 345
310 338 338
308

AccI |
DdeI |
AluI |
AluI |
HindIII |
AluI |
PvuII |
AluI |
RsaI |

FIGURE 3A

G06F 50/00

346 AAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTGTGTGTGACAAATATAATTCGGCCGGTATGGTTT 414
MspI
HpaII
HaeIII
||
403
404
404

415 GGTTAAGACTTGTGAGAGACGTGTGGGTTTTTTTGATGTATAATTAGTCTGTGTTTAGAACGAAACAA 483

484 GACTTGTTGNGTATGCTTTTTTTTAACTTGAGGGGGTTTGTGTGTGTAGTTAGGAACCTTGTCT 552
Tth111I
|
547

553 CTTTCTCTCAAGATCTGATTGGTAAGTCTGGGTGGTAGTACTGTTTGGTTTAAATTTGTTGACTATT 621
Sau3AI
BglII
|
564
564
ScaI
RsaI
|
593
593

622 GAGTCACTGTGGCCCATTTGACTTTTAAATTAGGCTGGTATATTTTGTGTTTAAACCGGCTGAGATAG 690
HinfI
|
623
634
646
HpaII
DraI MspI DdeI
|
673
678
683
678

FIGURE 3B

Sequence 3754360

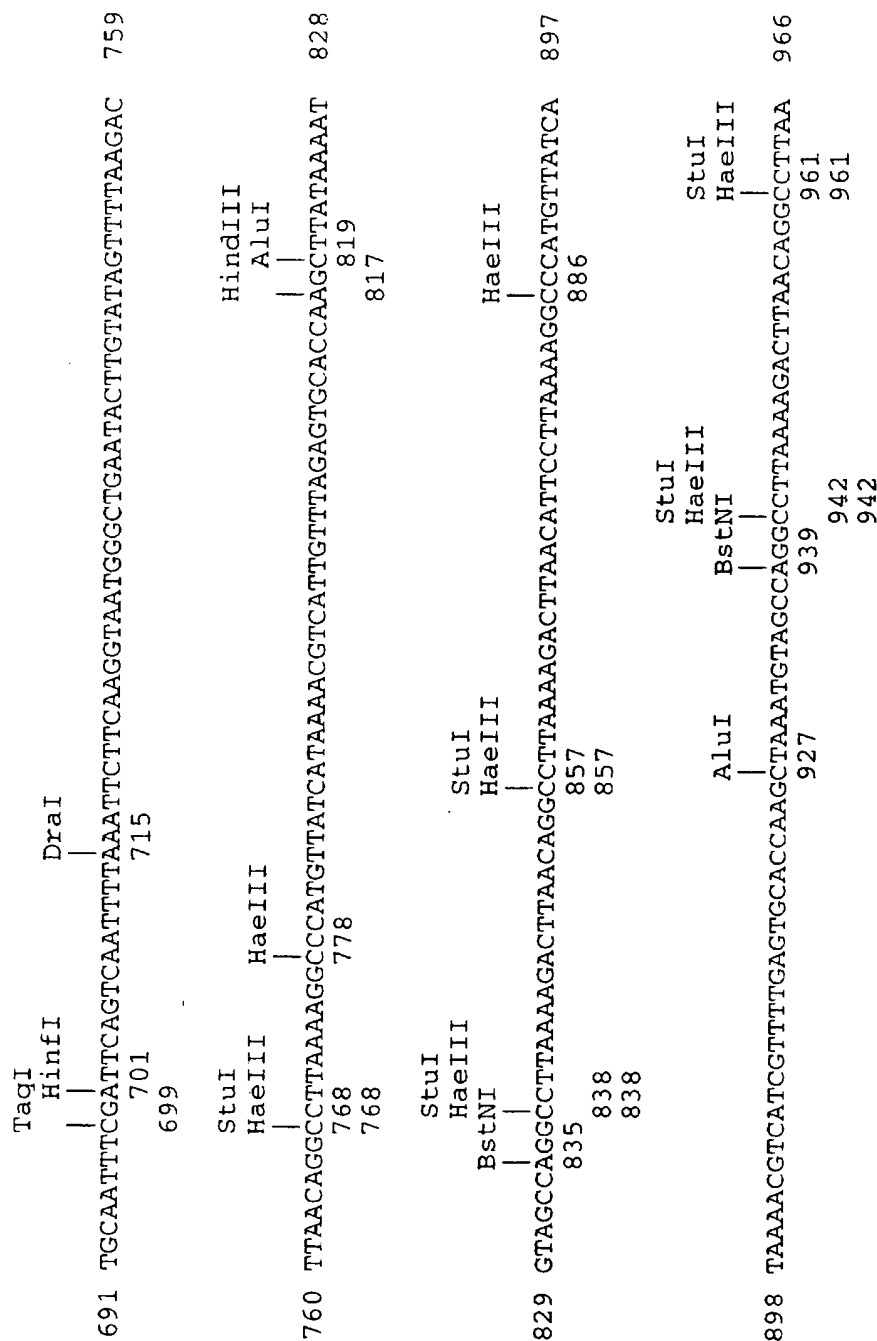


FIGURE 3C

006750-94672560

1174 TGTGTTCCAGATCGCTCTGATCATACTTCTTTTAGATCATTTGCTCTCTGATCTGTTGCTTGATGTTT 1242
1184 1193 1210 1224
Sau3AI BclI Sau3AI Sau3AI
1243 GTTAACCTCTCCACGCATGTTTGATTATGTTGAGAAATTAGAAAAAATGTTAGCTTTACGAAATCTTTAG 1311
1243 1296 1303
HincII AluI HincII
1312 TGATCATTTCAATTGGATTGCAATCTTGTGTGACATTTGAGGCTTGTGTAGATTTTCGATCTGTATTCA 1380
1313 1369 1368
Sau3AI BclI TaqI Sau3AI
1381 TTTTGAATCACAGCTATAAATAGTCATTTTGAGTAGTAGTGTGTTTAAATGAACATGTTTGTGTATTGA 1449
1386 1394 1425
HincII AluI DraI
1450 TGGAACAAACAGGCAGCAACACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTC 1518
AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu
1496

FIGURE 3E

CGGATGAGG

1519 TCCTTCAACCTCCGCCGTTCAATCCCACTCGTTTCTCAATCTCCTCGCGGTATGTTCTCATCTCTCAG 1587
SerPheAsnLeuArgSerIleProThrArgPheSerIleSerCysAla 1568
TaqI 1584
AluI 1597
RsaI 1601
HaeIII 1648
AlaLysProG 1648
1588 CATTATTTTCGAGCTTGCTTGTCATGCTACTCTCTCTAATTGCTCTATTGGTTTATTAGGCCCAACCAG 1656
1601 1616
1597
DdeI 1676
AluI 1695
1657 AGACGGTTGAGAAAGTGCTTAAGATAGTTAAGAAGCAGCTATCACTCAAAGACGACCAAAGGTCGTTG 1725
luThrValGluLysValSerLysIleValLysLysGlnLeuSerLeuLysAspGlnLysValVala
1676
Sau3AI 1743
HinfI 1756
TaqI 1763
1726 CGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGACACTGTAAGTCATCAATCATCTCTTATG 1794
laGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThr
1743 1756 1763
DdeI 1837
SphI 1852
1795 TGAATAAAGAGAACTTGAAGAGTTGTTTTTAACATATTAACTGAGTGTGTCATGCAGGTGAGATA 1863
ValGluIle 1852

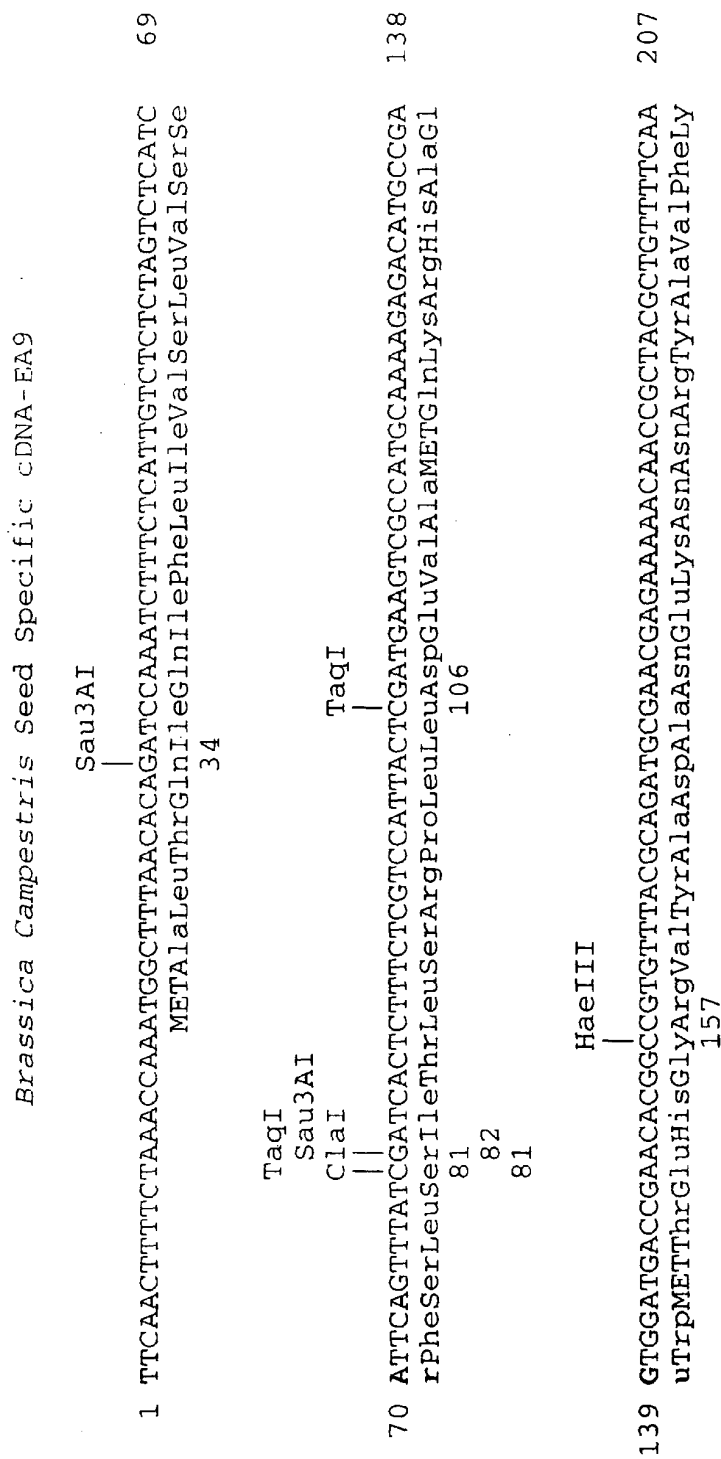
FIGURE 3F

006750-9464360



FIGURE 3G

006750-94642560



Complete nucleotide sequence of *B. campestris* cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIGURE 4A

CCGTCGAACTAAACCGCTTAAATGACGTTCAATCCGGACTAACGTTTAAACTCGCGGTGAA

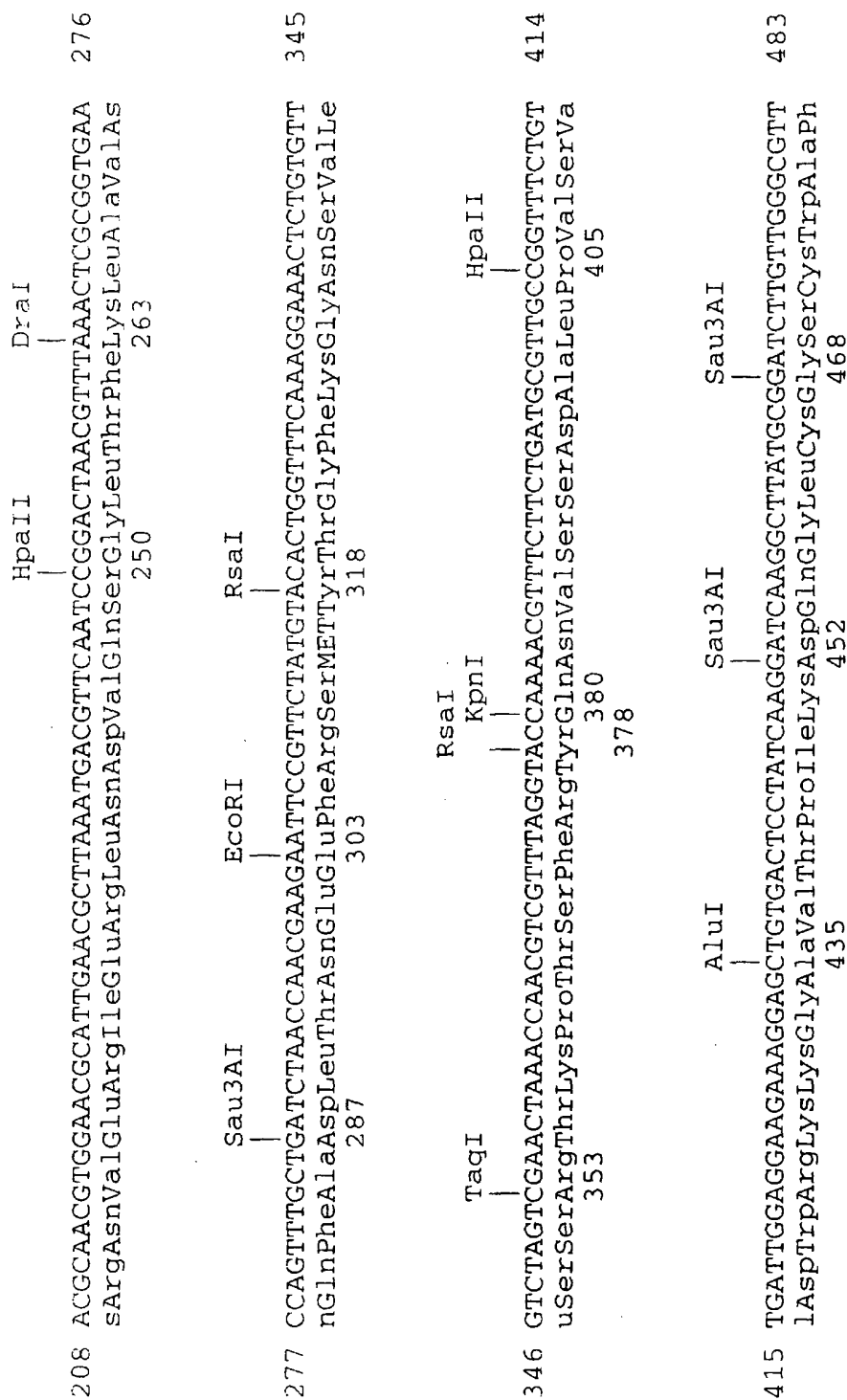


FIGURE 4B

006F50" 9h6h2560

PvuII
AluI
|
484 TTCAGCTGTTGCGGCTATAGAAAGGAGTAGCACAGATAAAGAAAGGAAACTCATTTCTTTGTCTGAACA 552
eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGlu
489
489
TaqI
SalI
HincII
AluI AccI
| | |
553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGGCGGTTTGATGGATACAGCGTTTAACTA 621
nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy
557 562
560
561
562
622 CACAATAACTATTGGCGGCTTAACCTCTGAATCAAAATTATCCTTATAAAGCACAAACGGCAGCTTGCAA 690
rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyrProTyrLysSerThrAsnGlyThrCysAs
HpaII
|
691 CTTCAATAAACTAAACAGATAGCAACTTCTATCAAAAGGTTTTTGAGGATGTCCCGGCTAACGATGAGAA 759
nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy
744

FIGURE 4C

006750-94642500

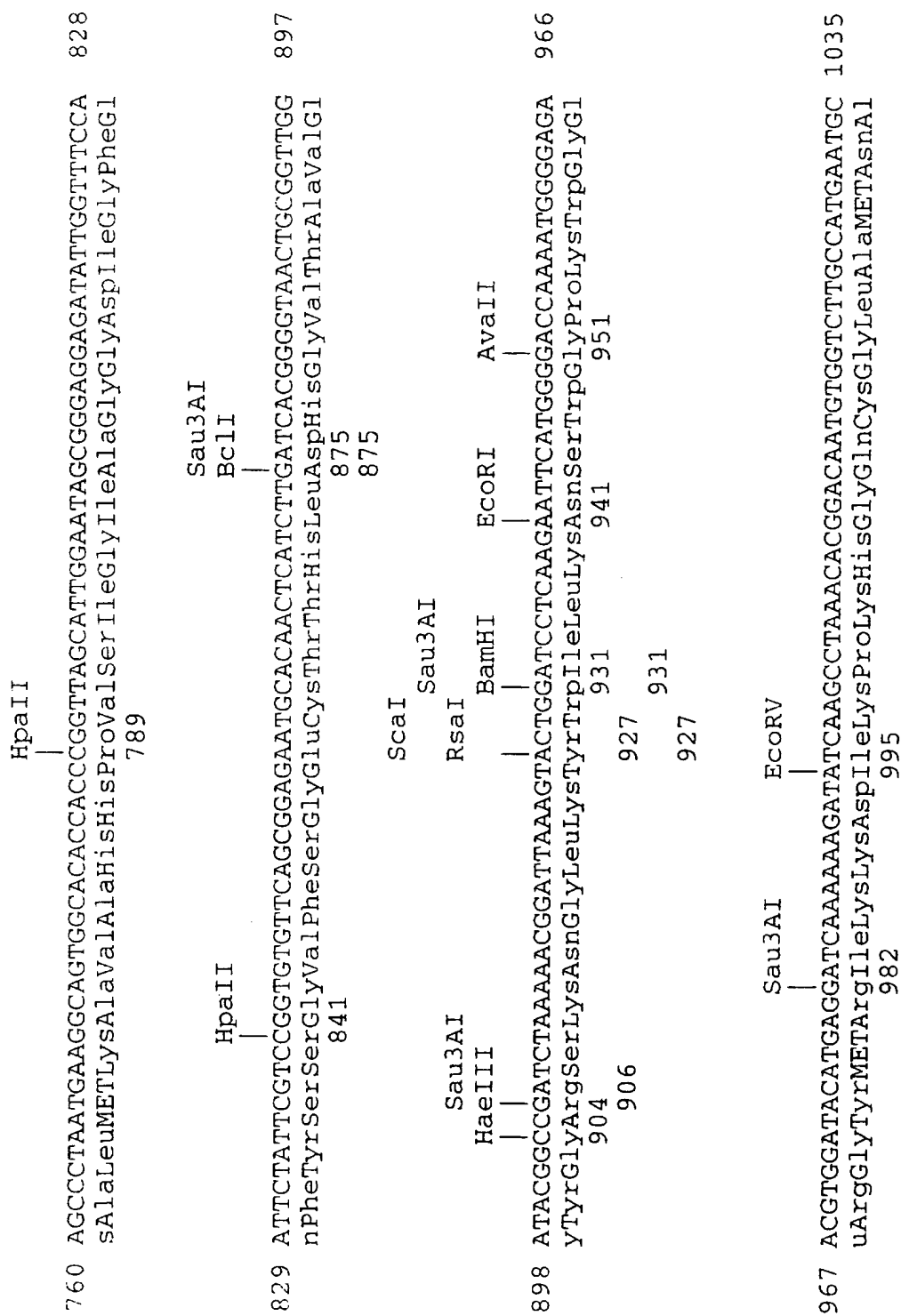


FIGURE 4D

CCGCGTACCCCAACTATATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAAATAAAATGTTGTGTGG 1104

1036 TTTCGTACCCCAACTATATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAAATAAAATGTTGTGTGG 1104
aSerTyrProThrMET
1041
RsaI |
HpaII |
HindIII |
AluI |
1073 1081
1079

1105 TTATAATTTAAGACTCTGTTGCATGTAATTGTGAAATGGTAAGTTTATGTGATGC AAAAGATTTGATA 1173
1174 AAAAAAAAAAAAAA 1186

FIGURE 4E

3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51
3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102
3H11 CAGAATCCTTCATCATAAAATAATATCAAATGCAAATCTATTTTTTCTAC 153
3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
TGCTCATCAATTAGCAATTAATCC
3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe
3H11 GTTGTTCCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTGAAAATG 306
2A11 GTTGTTCCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTGAAAATG
ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET
3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET
3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer
3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAAGGAGAAGACG 459
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAAGGAGAAGACG
AsnSerAspCysIleGlyIleThrLeuCysGlnPhyCysLysGluLysThr
3H11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro
3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA
3H11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATGTGAATAAAGGGATACATAT
3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT
3H11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATCCACATTAAT 714
2A11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTC
3H11 TCACGTATTTATTTCACTTATGATACGTATTTTGTTCCTTTGCGGTAAAA 765
3H11 AAAAAAAAA 774

FIGURE 5

(a)

2A11

PA1b

Chick pea
inhibitorLima bean
inhibitor α_1 -antitrypsin

V	M	A	L	R	D	I	P	P	Q	E	T	L	L
V	C	S	P	F	D	I	P	P	C	G	S	P	L
V	C	T	-	K	S	I	P	P	-	-	-	-	Q
L	C	T	-	K	S	I	P	P	-	-	-	-	Q
L	G	A	I	P	M	S	I	P	P	E	V		

↑

(b)

2A11

PA1b

Barley chloroform/
methanol-soluble
protein dWheat α -amylase
inhibitor 0.28

Wheat albumin

Millet bi-functional
inhibitorCastor bean 2S
small subunit

Napin small subunit

T	N	I	L	G	L	C	N	E	P	C	S	S	N	S	D	C	I
G	S	P	L	C	R	C	I	P	A	G	L	V	I	G	N	C	R
T	N	L	L	G	N	C	R	-	F	Y	L	V	Q	Q	T	C	A
V	S	A	L	T	G	C	R	-	A	M	V	K	L	Q	-	C	V
V	P	A	L	P	A	C	R	P	L	-	L	R	L	Q	-	C	N
N	N	P	L	D	S	C	R	W	Y	V	S	A	T	K	R	A	C
Q	Q	N	L	R	Q	C	Q	E	Y	I	K	Q	Q	V	S	G	Q
A	Q	N	L	R	A	C	Q	Q	W	L	N	K	Q	A	M	Q	S

FIGURE 6

006F50" 57642560

2A11 GENOMIC

CTCGAGCCCT	TTAAAAAGTA	TAGTCAATAT	TTACGGTGAC	CGTGAATTTC	TTAATTATCA	60
TATATAATTT	AAAAGAAATC	ATGATCACAT	TCTACTGATG	AGAACATGTG	CTAATCAAGG	120
GAAACATGG	ATGTGAAAAA	TACTTTTGT	TAAAAGTAAA	AAAAAATGTG	AAATTTTGT	180
AGTTATTAC	TACCTATACA	TTATTTGAGC	ATGTGCAAAC	TTTACAAATA	CCTAATAGAA	240
GATTTTCACC	TGCCCTGTATA	TATGTAAATT	AATTATAATG	AACACTCTCA	CATAAAATAA	300
TTATCAGTAT	ATACATTAAAT	ACTTGCCCTC	CACAATGAAT	TAAATAAAAT	GTAGAACATG	360
ATCTACACTT	CAATAAAACT	AAGACCATAA	AGAATAAATT	CAAAATATAC	ACATGTCAAC	420
AAATAAATTAT	TTGCATATTA	TATTAACCTA	CTAAACAATC	TTTACTTTTG	AAATATAAAA	480
ATAATCAAAGT	TATAAGTCTG	CTCAAAGTAA	AGCACTTGTT	AGACTCATCT	GATTTTGAGA	540
AGGTAAGCAA	ATTGATGGTG	CATAATAGTC	ACAAGTAAAA	TATAAAATAG	ATTTTCATTAG	600
TAAAATTGTT	TTTTACTTTC	TTTATATATA	ATTATCAATA	TCCTTCAATG	GTAGGTTAAT	660
TATATTGTTA	ACTTCTTGTT	GAATTAAAGC	AATAAGACAA	GAATATTAAA	GATAAAAGAA	720
CAATAAAAAAT	AGAAAGACTA	AGAGATAAGA	GTTTTCTTAT	TCTTCTTTCA	ATAAGTATCA	780
TCAAGTGTAT	ACAATATAAA	TTTTTGTATT	TTTGATCTAT	CTATTATATA	TGTTATATAT	840
AAGCATACAA	AAGATCAGTC	ATAAATATGA	CTTTAATCAT	GAAAAATAATG	AAAGAGATTA	900

FIGURE 7A

U96F50" 57674560

TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAAAAAAA GGGTTATCT TTATAATTGA 960
ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT TTTTTTAAAA AAATGGACAT 1020
TTACACTATA ATATTTTATA ACACTTTCCC TTAAACATCT AGGTATAAAT AATGAGTCTT 1080
GTCAAAATCT TAGTAGGAAA AATTCTGTGA AATTTTITTA GTGAAAACAA ATGATAATAA 1140
TATCTTGAAT ACTCAATTATT TGTGTCTCA TTAAAAATCT TATCTGACCT ATAAAAATAA 1200
TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAAATTA GTATAATTAT TAGTGAATAT 1260
TTAATTAACA TAATTGTATA CTAAGGGGCC TATAAATGG ATTCTTCTCA AAGAAAAATA 1320
AAATCACCAC ACAACTTTCT TCTTCTGCTC ATCAATTAGC AATTAATCCA AAACCATT 1378
ATG GCT GCC AAA AAT TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT 1426
MET Ala Ala Lys Asn Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val
CTT TTG ACG ACC ACT TTA GGTTCAACAAC ACTTCTCCCT TATTTTGTTT 1474
Leu Leu Thr Thr Thr Leu
TCTTAATTTC TTGGAAGTCA TATGCATGTG TTGGGTATCA TGGTATATAT ATAAAGGAAA 1534
ATATTTTCT TAATTACTGG TTTTCTAATG TTTGGTAGGT AATCGGAAAT TATTATGAGA 1594
TAATGAACCT GCAAAGTCAT TATTATATAA CTTTTTTTTT ATACTTTGAT TTAAGAATTC 1654
ATTTTCTCA TTTTATATAA ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA 1714
CACACCCCTAA GACATTACAT ATATATATAT ATACACCCCTC CGTTTATAT TACTTAATGC 1774

FIGURE 7B

DDBTSD: 57674560

CTATTGAGTT GGGCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT ACTAAATTAA 1834
CCTATGCTTT AAGACTCTAA ATTTGGCTAT TACTATTTTA CGTTGTAATT TAATGACAAA 1894
CATTTCAATA TGAATAAGT CTGAACCTAA TTAGACAGAC GATCTATAG TTTGCTTACT 1954
AATGATTTCAT AGCTATATAT TTGGAGAGGA GAGAGACAAA CGATATTAAAG AAAGGGAGGA 2014
GAGAGGCGAG GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA 2074
TACTTTTGAT TATTATTTT ATTATATGTA CGTTTACATT ACAGTTTTCG AATTCTTACA 2134
TTAATCTTAA TCATAATATA TACA GTT GAT ATG TCT GGA ATT TCG AAA ATG CAA 2188
Val Asp MET Ser Gly Ile Ser Lys MET Gln
GTG ATG GCT CTT CGA GAC ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG 2236
Val MET Ala Leu Arg Asp Ile Pro Pro Gln Glu Thr Leu Leu Lys MET
AAG CTA CTT CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC 2284
Lys Leu Leu Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT TGT AAG GAG 2332
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe Cys Lys Glu
AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT ACA TGC AAC CTG TTG CCT 2390
Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg Thr Cys Asn Leu Leu Pro
TGA ACAATATCAA TGATCTATCG ATCGATCTAT CTATCTATTT ATCTGTCTCT 2433
GCGCGTATAG TGTGTCTGT ACCTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT 2493
CTAGATATAT TCTAGGTAAT GTCCTATTGT ATTTAAATTT TGTAGCAATG ATTGTTTGAA 2553

FIGURE 7C

DDBP SEQ 9464350

TAAAAACATA	CCATGAGTGA	AATAATTATT	CCACATTAAAT	TCACGTATTT	ATTCTACTTA	2613
TGATACGTAT	TTTTGTTCCT	TTCGCGTAGA	TTTTTGATCC	TTTTCCCTTT	TGAATATTAA	2673
ACATTAAACA	CAAATAATGT	TTATTAAATT	AAGTTAATAT	TTTTATTTAG	CTATTTATAT	2733
TTTTTATTGA	AATCAAACTT	GATAAATATT	TATAAAGATA	ATTAAACAAGT	AATGTGACAC	2793
TAACACCATG	TAATATTATC	TTGTCGTTAT	TTATGATAAT	ATTTTAAAAAT	TATAATTTCAT	2853
GTAAAAAAAT	TATTAAAAAA	ACATACTTTT	AAAAAGTGAG	TTAGCCTCCG	CTACCCACAT	2913
ACTTATGAAT	TGGACTAGTT	GTTTTTTGAC	CCACAAAAAG	AATGGGCTAA	TTAAACCTGA	2973
CCTATCAAAT	TTCAGAAATCT	GCATAGATTA	GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	3033
ACAAAATATC	AACAAGGACG	TTATGTAAAG	ATGTTTAAAG	AGGAAAAAAG	ATTTCATAATA	3093
CATATGGACT	TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCCTGCTT	AGTTTGTGTA	3153
TCATTAACTT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTTAA	ACTTACAGAA	3213
AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC	TTTAGTACTT	AAACTACATG	3273
AAAATTTAAA	TATCCTTTTA	ACATCTTTGA	AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	3333
CACCTTGGAC	GTGGCCGGCA	CTCAAGAACC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	3393
GACTGACTAC	AAGCGGAAGG	CTAACTTAAG	TATACAAAAAG	CTTAAAACTG	AATAAAAATA	3453
ACTTTACAAG	GTTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT	TCAACTAGCC	3513

FIGURE 7D

ccttgaagac

ATAAAATAGA CAACTTTTAGT CTTTAAAACA TTTAATAAAA TAAATGCAAA ATATAGACTC 3573
CTTAACTAAA CTGACTATCT ATGGAGCCTC TAATTGATAA AGATGGAAGT CGGGACAAGA 3633
CCACGACATC CTGACTAAAC TGAGAAAGTAA ATAAAATCCC CCGGAAAAAA AGGAGCCTCA 3693
CCATGGGCTAA CTCGAACTCG GGGATATATC AATGAAGCTC CTGTTGATGA TCTTGAAGAC 3753
ATGTCTCTGC ATCATCAAAA AGATGCAGGC CAAATGGCTC AGTACGTAAA ATGTACGAGT 3813
ATGTAAGGGA AATTCTAAAG TATAACATAA GCTTGATACT TGAATAAAA GAAACATACT 3873
TACCTCTTTT CAACTCAACT CAAATTAAGA ATAAGATACT CAACTCAAAG ATTAGGTATT 3933
CAACGCAAAT ATGGCACTCT ACTCAATGAA GTACAAAATTA ACTCAGGATA CTCGACTTAA 3993
GATACTCAAC TCCCGACACT CAACTGAACT CATTCAATA TAAAGCAGCT TAAAAACAAGT 4053
TCAGTATAAA GTAAAGTTGT TTAAAAACAT GATGTCAACT CTGTGTGTAT AATAAGGGAT 4113
ACAACATAAC TTTGAAATGT ATATAAAAAAT ACAATTAACT GATGTATATA AAAATACATT 4173
AATCTATGGG AGATTCTCTA ACCGACAACC ATCACTTAAG GGCTAAGATG ATGATATAGC 4233
GATCTACCGC ACGCTGCCAT CGCATCTTAT ACCCGGCCAA AGGTATAAGA CCTGAACCTGC 4293
CTAATGAATC CACTAATAAA CTGTTAAAAG GAATCATCTA AAAAGTATGA CCTTTTCTA 4353
CCCATAGTGG CTAACATGGT TTATGGGGGC TGTGAGTTAT CTGAACCTCTC CCCCATATCG 4413

FIGURE 7E

605450-4656

GTGCTCAATA CTACTCCAAA AAATATACTG CTCTTATGTT TAAAAACATA CTGATTCTGT 4473
GGTTTGAAAT TATTGCTTAA AGCTTAGATT TTTGAAAAGC TCTCTTTTGA AAATCGTAGT 4533
TTCCTTTTTC TTCTATTAAA GCTAGACATA GGCTATGTAG AACTCTAGCT TACCTTCCCTT 4593
CTCAAAAAGTT TGAAAAACATT TGCTTAGATT CTAGGGACT ACTTAGTTCC CTGTGTGGAA 4653
TTC 4656

FIGURE 7F

10	20	30	40	50	60
AAGCTTCTTA	AAAAGGCAAA	TTGATTAATT	TGAAGTCAAA	ATAATTAATT	ATAACAGTGG
70	80	90	100	110	120
TAAAGCACCT	TAAGAAACCA	TAGTTTGAAA	GGTTACCAAT	GCGCTATATA	TTAATCAACT
130	140	150	160	170	180
TGATAATATA	AAAAAAATTT	CAATTCGAAA	AGGGCCTAAA	ATATTCTCAA	AGTATTCGAA
190	200	210	220	230	240
ATGGTACAAA	ACTACCATCC	GTCCACCTAT	TGACTCCAAA	ATAAAATTAT	TATCCACCTT
250	260	270	280	290	300
TGAGTTTAAA	ATTGACTACT	TATATAACAA	TTCTAAATTT	AAACTATTTT	AATACTTTTA
310	320	330	340	350	360
AAAATACATG	GCGTTCAAAT	ATTTAATATA	ATTTAATTTA	TGAATATCAT	TTATAAACCA
370	380	390	400	410	420
ACCAACTACC	AACTCATTA	TCATTAAATC	CCACCCAAAT	TCTACTATCA	AAATTGTCCT
430	440	450	460	470	480
AAACACTACT	AAAACAAGAC	GAAATTGTTC	GAGTCCGAAT	CGAAGCACCA	ATCTAATTTA
490	500	510	520	530	540
GGTTGAGCCG	CATATTTAGG	AGGACACTTT	CAATAGTATT	TTTTTCAAGC	ATGAATTTGA
550	560	570	580	590	600
AATTTAAGAT	TAATGGTAAA	GAAGTAGTAC	ATCCCGAATT	AATTCATGCC	TTTTTTAAAT
610	620	630	640	650	660
ATAATTATAT	AAATATTTAT	GATTTGTTTT	AAATATTAAA	ACTTGAATAT	ATTATTTTTT
670	680	690	700	710	720
TAAAAATTAT	CTATTAAGTA	CCATCACATA	ATTGAGACGA	AGGAATAATT	AAGATGAACA
730	740	750	760	770	780
TAGTGTTTAA	TTAGTAATGG	ATGGGTAGTA	AATTTATTTA	TAAATTATAT	CAATAAGTTA
790	800	810	820	830	840
AATTATAACA	AATATTTGAG	CGCCATGTAT	TTTAAAAAAT	ATTAAATAGT	TTGAATTTAA

FIGURE 8A

[illegible]

850 860 870 880 890 900
AACCGTTAGA TAAATGGTCA ATTTTGAACC CAAAAGTGGA TGAGAAGGGT ATTTTAGAGC
910 920 930 940 950 960
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG GATAATTTTG
970 980 990 1000 1010 1020
TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC CCTTCTTTAG TTTATAGACT
1030 1040 1050 1060 1070 1080
ATAGTGTTAG TTCATCGAAT ATCATCTATT ATTTCCGTCT TAAATTATTT TTTATTTTAT
1090 1100 1110 1120 1130 1140
AAATTTTTTA AAAATAAATT ATTTTTTCCA TTTAACTTTG ATTGTAATTA ATTTTTAAAA
1150 1160 1170 1180 1190 1200
ATTACCAACA TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTTTA
1210 1220 1230 1240 1250 1260
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA AAAATTGAGA
1270 1280 1290 1300 1310 1320
CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAACTCT TTCGTCTAAA TATCTCTCAT
1330 1340 1350 1360 1370 1380
CCAAACTAAT ATAATACCCA TTATAATTAA CCATATTGAC CAACTCAAAC CCCTTAAAT
1390 1400 1410 1420 1430 1440
CTATAAATAG ACAAACCCTT CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTTCA
1450 1460 1470 1480 1490 1500
ATAGACAAGT TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT
1510 1520 1530 1540 1550 1560
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG CAATGTTATT
1570 1580 1590 1600 1610 1620
GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG AACAAGAATT TGCTCATGAT
1630 1640 1650 1660 1670 1680
TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA AATATTGAAA GCAACAATAA TATTGACAAG

FIGURE 8B

1690 1700 1710 1720 1730 1740
GTTGATAAAA ATGGGATTAA AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA
1750 1760 1770 1780 1790 1800
AAAACATATG ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT
1810 1820 1830 1840 1850 1860
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA AGTAGAAAAT
1870 1880 1890 1900 1910 1920
TATTTTCTCG TTTT TAGTAA TTAAAGGTGA AAAATGAGTT TTCTCGTAAG CGAGGAAAGT
1930 1940 1950 1960 1970 1980
CATTTTCCAT GGAAGTGTAT TTTTTTTTTT CTTTAAATAA CGTCATAGTA TTTGCTATAC
1990 2000 2010 2020 2030 2040
TCAAGAATAA GACACTATTA TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG
2050 2060 2070 2080 2090 2100
CTAATATAAC TATCAATTTT TTATATGTAT ATTTTTC AAC CAAAATAACA AAGCGTAATC
2110 2120 2130 2140 2150 2160
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT TATTTAATTT
2170 2180 2190 2200
TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT CGAATTC

FIGURE 8C

005750-94642560

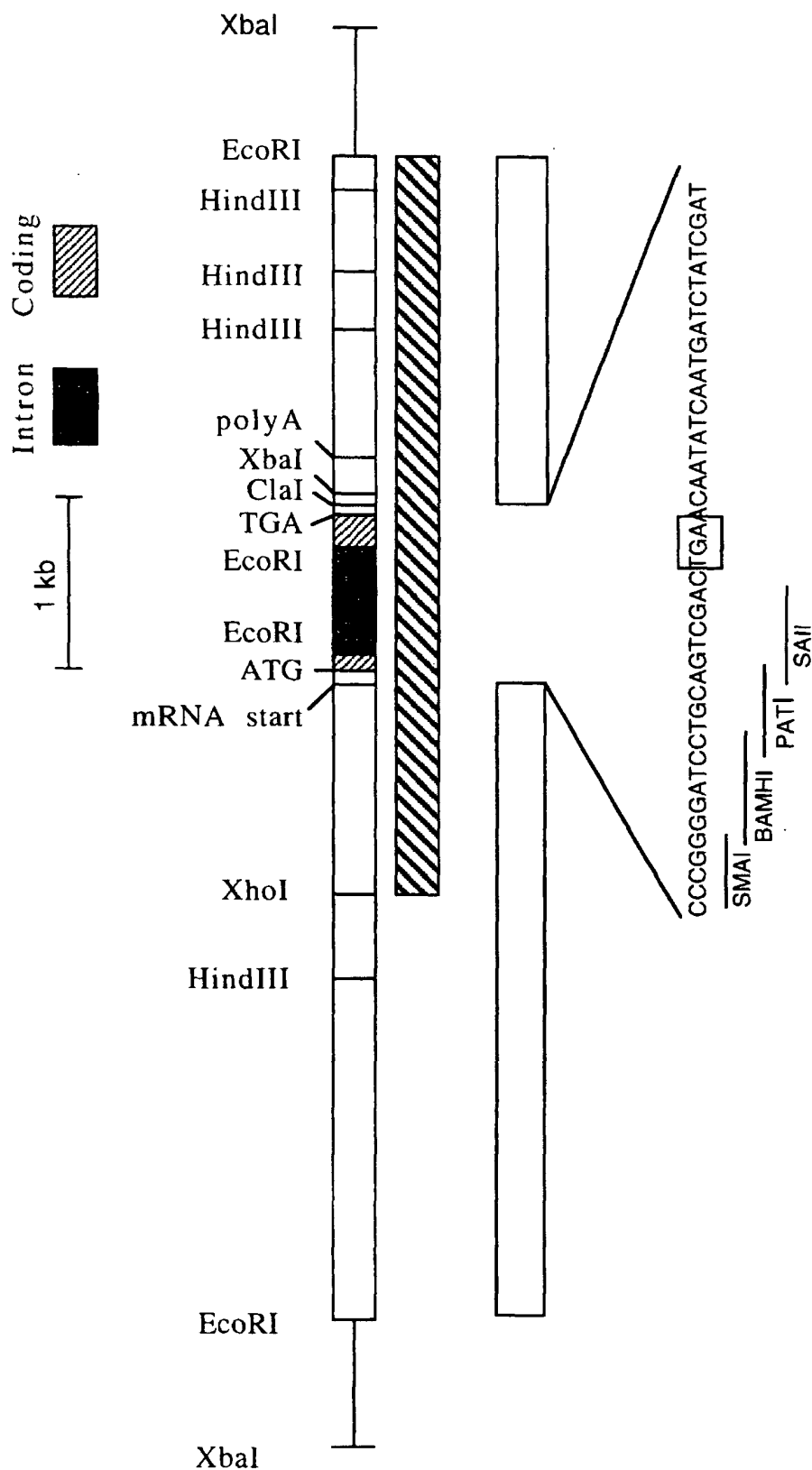


FIGURE 9

006T50" sh6h.560

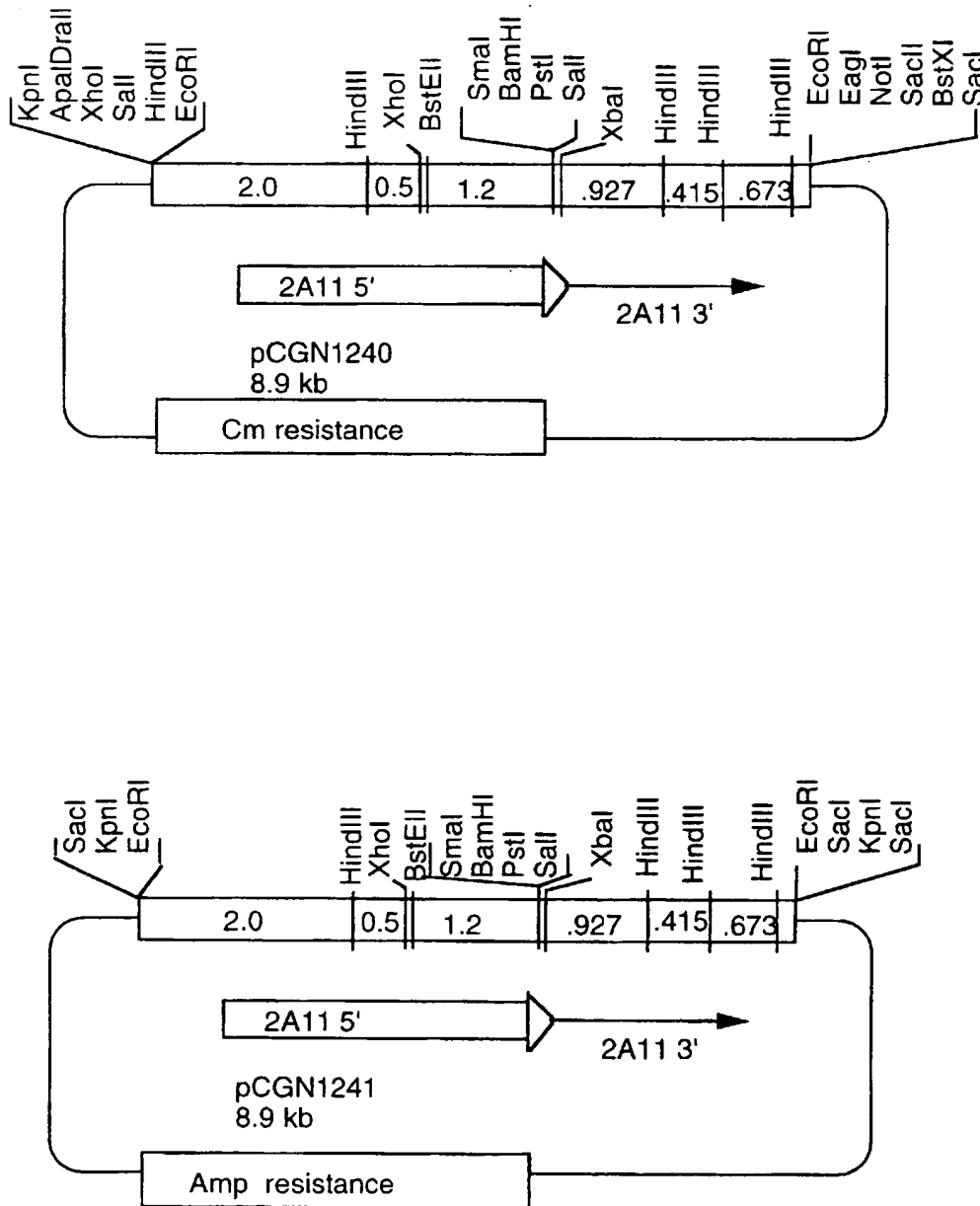


FIGURE 10A

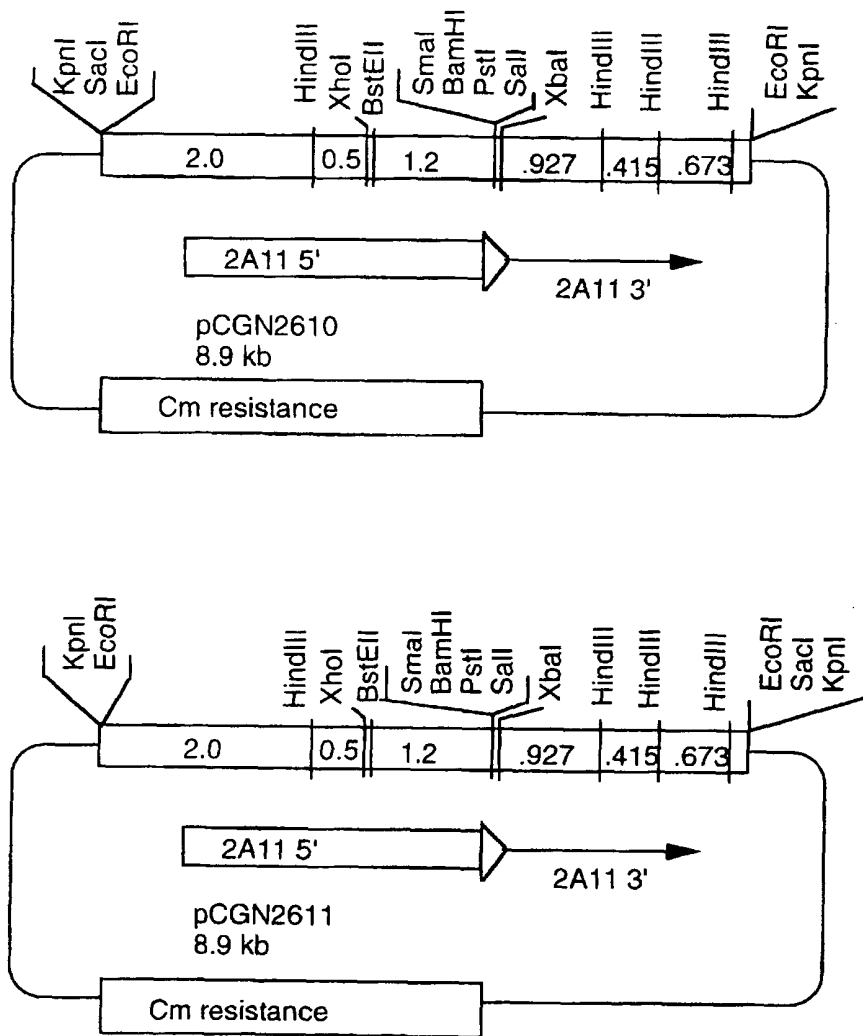


FIGURE 10B